APPLN. FILING DATE: APRIL 19, 2001
TITLE: PEPTIDE SEQUENCES SPECIFIC FOR THE
HEPATIC STAGES OF P. FALCIPARUM BEARING...
INVENTOR(S): CLAUDINE GUERIN-MARCHAND ET AL
APPLICATION SERIAL NO: 010830-116
SHEET 1 of 18

5')	1	SDLEQERRAKEKLQEQQ
	18	SDLEQDRLAKEKLOE00
	35	SDLEQERLAKEKLQEQQ
	52	SDLEQERRAKEKLQEQQ
	69	SDLEQERRAKEKLQEQQ
	86	SDLEQDRLAKEKLQEQQ
	103	SDLEQERRAKEKLQEQQ
	120	SDLEQERKAKEKLQEQQ
	137	SDLEQERLAKEKLQEQQ
	154	SDLEQERRAKEKLQEQQ
	171	SDLEQERRAKEKLQEQQ
	188	SDLEQERRAKEKLQEQQ
	205	RDLEQ
	210	RKADTKKNLERKKEHGDILAEDLYGRLEIP
	240	AIELPSENERGYYIPHQSSLPQDNRGNSRD

270 SKEISIIEKTNRESITTNVEGRRDIHKGHL 300 EEKKDGSIKPEQKEDKS 316 (3')

AAAGCGATCTAGAACAAGAGGACGTGCTAAAGAAAAGTTGCAAGAACAAC **AAAGCGATTTAGAACAAGATAGACTTGCTAAAGAAAAGTTACAAGAGCAGC AAAGCGATTTAGAACAAGAGACTTGCTAAAGAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC AAAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA AAAGCGATCTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGATAGACTTGCTAAAGGAAAGTTACAAGAGCAGC AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGAGACTTGCTAAAGAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGAGAGGCGTGCTAAAGAAAAGTTGCAAGAACAAC AAAGCGATTTAGAACAAGAGACGTGCTAAAGAAAAGTTGCAAGAGCAGC** AGGAAGGCTGATACGAAAAAAATTTAGAAAGAAAAAGGAACATGGAGAT CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACCT CAGGACAACAGGGGAATAGTAGAGATTCCAAGGAAATATCTATAATAGAA **CATAAAGGACATCTTGAAGAAAGAAGATGGTTCAATAAAACCAGAACAA** ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT 950 (3.) AAAGAGATTTAGAACAA AAAGAAGATAAATCT 358 409 460 562 613 307 511 630 783 834

TITLE: PEPTIDE SEQUENCES SPECIFIC FOR THE HEPATIC STAGES OF P. FALCIPARUM BEARING... INVENTOR(S): CLAUDINE GUERIN-MARCHAND ET AL APPLICATION SERIAL NO: 010830-116 SHEET 3 of 18

RDELFNELLNSVDVNGEVKENILEESQVNDDIFNSLVKSVQQEQQ HNVEEKVEESVEENDEESVEENVEENVEENDDGSVASSVEESI ASSVDESIDSSIEENVAPTVEEIVAPTVEEIVAPSVVEKCAPSVE ESVAPSVEESVAEMLKER

GAA AGT CAA GTT AAT CAA CAA GAA CAA CAA AGA AGA AA ATG ACG AAG TAG ΓAG AAA AGT AAG AAG AAG SAA GAT AATAAG A GAG CAC CAC AAG ACG TTG TTG

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### FIGURE 4

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7295-NRI 7295-NRII 7295-Rep

DELFNELLNSVDVNGEVKENILEESQ LEESQVNDDIFSNSLVKSVQQEQQHNV VEKCAPSVEESVAPSVEESVAEMLKER

NSRDSKEISIIEKTNRESITTNVEGRRDIHK

LSA-TER

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### NUCLEOTIDE SEQUENCE OF THE LSA GENE 5' END

(NON-CODING 5' END)

1 AAAGTATACATCTTCCTTCTTTACTTCTTAAA

(CODING 5' END, UNIQUE)

33	ATGAAACATATTTTGTACATATCATTTTACTTTATCCTTGTTAATTTATTG
84	ATATTTCATATAAATGGAAAGATAATAAAGAATTCTGAAAAAGATGAAATC

135 TAAAATCTAACTTGAGAAGTGGTTCTTCAAATTCTAGGAATCGAATAAATGA 186 GGAAAATCACGAGAAGAACACGTTTTATCTCATAATTCATATGAGAAAACT

237 AAAAATAATGAAAATAATAAATTTTTCGATAAGGATAAAGAGTTAACGATGT

288 CTAATGTAAAAAATGTGTCACAAACAAATTTCAAAAGTCTTTTAAGAAATCT

441 AAGGGCAAGACGAAAACAGACAAGAAGATCTTGAAGAAAAAGCA

(CODING 5' END, repetitive)

492 GCTAAAGAAAAGTTACAGGGGCAACAAAGCGATTCAGAACAAGAGAGACGT

543 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT

645 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT

747 GCTAAAGAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACGT

798 GCTAAAGAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACTT

849 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGATAGACTT

900 GCTAAAGAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACGT

951 GCTAAAGAAAGGTTGCAAGAACAACAAAGCGATTTAGA 988

LSA.5'/ATG - -> 1-phase Translation

linear ... AAGCGATTTAGA ATGAAACATATT b.p. 926 seguence

SAT his AGA arg AAG lys CTT val phe AAG TTG leu CAC GAT asp lys AGT ser asn AAA 1ys AAA ATA ile AAC ΣL phe lys AAT asn LTG leu ser AAG 1ys TTA 77 ohe phe len GAG glu len AAA 1ys AAAasn AAA lys lys AAT ATA ile AAT ACA asn his asn AAT asn SAC AATthr AAT GAA ATC ile asn GAA AAT asn CAA glu GTT GAA glu GAA len glu TCA AAA E ser lys GTG val ATC ile asp GAG glu AAT GAT asn leu H phe AAA lys AAT asn AAT asn AAT asn TAC tyr GAA glu 51 ATA i 1e 71 AAA lys 91 AAA lys 111 ATA CGA ATA TCA TTT ser arg asn /al ser AAG AAT asn AAT lys 271 AAT asn 331 GAG 151 asn AAA lys AGG 6AG glu ζY arg ser ser TCT ATA ile tyr TCT ATG TAC TAT tyr ser met val TTG leu ATA ile AAT asn Z ACG ser thr gly GGT Τζ ile AAG lys asn TTA ser AAT leu leu AAA CAT AAT GGA gly 41 ser ٦ij۶ GAG SAT asn / gly / TCT ser / AAA lys **GGT** ATA ile 121 AGT ser 181 TTA 1eu 241 GAT

## FIGURE 7A

### 56G gly 36G AGC ser GAA AGA arg AAA Lys TTG AAA lys CAA TTA GAG glu CAG gln GCT ala AAG lys CAA ATT ile TTA GAT CAA CGT GAA glu GAA glu AGC ser GAA glu AGA arg AAA 1ys TAT AAG lys CAA gln TTA AAA 1ys GAA glu CAA GAG glu GCT CAA gln AAA lys GAT CAA gln AAA 1ys TTG leu CGT AAA lys GCT ala GAA glu AGC ser GAA glu AGA arg AAG lys GAT GAA glu CAA CAA gln TTA GCA ala GAG glu GAC AAA 1ys TTG leu AAA 1ys CAA gln asp CAA GAT GAT GAA glu GCT ala AAG lys SAA AGC ser GAA glu 131 6AT 6AT 151 151 171 171 171 171 191 6AA 8GN CAA 8GN 7231 CAA 8GN AAAT aasn CTT CCTT leu AAAA AAAA Iys / CCAA gIn ser ATA ile GAA glu CAA CTT GAA glu CAA gln CAA GAA glu CAA gln CAC his AGA arg AAA 1ys CAA TTG leu GAA glu AGA arg TCA GAG glu **GCT** ala AAG 1ys GAA glu AAC asn ATT ile GAT CAA SAA glu CGT arg CAA 121 TTA 141 141 5AA 5AA 161 161 ser 181 6AA 6AA 201 AGA arg 221 AAA Lys 241 FTG AAAA 1ys 1ys GAC GAC CCAA BIL GGG GGC AAG

## FIGURE 7B

APPLN. FILING DATE: APRIL 19, 2001

CAG gln GAT GAG glu AGC CAA gln CAA gln TTA TTA CAA gln GAT AAG lys GAA glu AGC GAA glu CAA gln CAA gln AAA 1ys TTG leu CAA gln AAG lys GAA glu GCT ala CTT leu GAA glu CAA gln AGA arg 4AA Lys TTG leu 271 GAG GBlu 291 201 GCT GCT 311 AGG CAA CAA gln CTT CTT leu / GAA 811 GAA GAA 871 AGA arg 931 AAA TTA leu GAT asp GCT ala GAT CAA gln CGT arg AGC GAA glu AGA arg CAA TTA GAG glu 261 CAA gln 281 6AT asp 301 CAA GAA GAA glu AGC Ser Ser GAA 781 CAA 841 841 CAA CAA gln 901 TTA

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### NUCLEOTIDE SEQUENCE OF THE LSA GENE 3' END

### (CODING 3' END, REPETITIVE)

- 1 CAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT
- 37 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT
- 88 GCTAAAGAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACTT
- 139 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATCTAGAACAAGAGAGACGT
- 190 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 241 GCTAAAGAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGATAGACTT
- 292 GCTAAAGAAAAGTTACAAGAGCAGCAAAGCGATTTAGAACAAGAGAGACGT
- 343 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 394 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACTT
- 445 GCTAAAGAAAGTTGCAAGAACAACAAGCGATTTAGAACAAGAGAGACGT
- 496 GCTAAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 547 GCTAAGAAAAGTTGCAAGAACAACAAAGCGATTTAGAACAAGAGAGACGT
- 598 GCTAAAGAAAGTTGCAAGAGCAGCAAAGAGATTTAGAACAA

### (CODING 3' END, UNIQUE)

- 640 AGGAAGGCTGATACGAAAAAAATTTAGAAAGAAAAAAGGAACATGGAGAT
- 691 ATATTAGCAGAGGATTTATATGGTCGTTTAGAAATACCAGCTATAGAACTT
- 742 CCATCAGAAAATGAACGTGGATATTATATACCACATCAATCTTCTTTACCT
- 793 CAGGACAACAGAGGGAATAGTAGAGATTCCAAGGAAATATCTATAATAGAA
- 844 AAAACAAATAGAGAATCTATTACAACAAATGTTGAAGGACGAAGGGATATA
  895 CATAAAGGACATCTTGAAGAAAAGAAAGATGGTTCAATAAAACCAGAACAA
- 946 AAAGAAGATAAATCTGCTGACATACAAAATCATACATTAGAGACAGTAAAT
- 997 ATTTCTGATGTTAATGATTTTCAAATAAGTAAGTATGAGGATGAAATAAGT
- 1048 GCTGAATATGACGATTCATTAATAGATGAAGAAGAAGATGATGAAGACT
- 1099 TAGACGAATTTAAGCCTATTGTGCAATATGACAATTTCCAAGATGAAGAAA
- 1150 ACATAGGAATTTATAAAGAACTAGAAGATTTGATAGAGAAAAATGAAAATT
- 1201 TAGATGATTTAGATGAAGGAATAGAAAATCATCAGAAGAATTATCTGAAG
- 1252 AAAAAATAAAAAAAGGAAAGAAATATGAAAAAAACAAAGGATAATATTA
- 1303 AACCAAATGATAAAAGTTTGTATGATGAGCATATTAAAAAATATAAAAATG
- 1354 ATAAGCAGGTTAATAAGGAAAAAGGAAAAATTCATAAAATCATTGTTTCATA
- 1405 TATTTGACGGAGACAATGAAATTTTACAGATCGTGGATGAGTTATCTGAAG
- 1456 ATATAACTAAATATTTTATGAAACTA<u>TAA</u> (stop)

### (NON-CODING 3' END)

1485 AAGGTTATATATTT 1498

LSA.3'.ALL -> 1-phase Translation

linear CAAGAACAACAA ... GGTTATATTT 1496 b.p. DNA sequence

SAA GAT CAA gln GT arg GAA glu CAA AGA arg GAA GAA glu AAA 1ys AGC ser T1G leu GAG CAA CAA CTA GCTala AAG lys CAG gln CAA TTG GAT asp GAA E leu glu AGA arg AAG lys GAG glu AGC ser GAA AAA lys CAA TTA GAT GAA glu CAA GCT ala CAA CAA gln AAA 1ys TTA GAT arg CGT GCT ala GAA glu GAA glu AGA AAG lys AGC arg ser GAA CAA GAG CGT TTA CAA CAA AGA arg AAA lys TTG leu CAA gln GAT asp gln GAG glu AAG 1ys GAA glu GCT ala GAA glu AGC ser / 11 GAA CAA e n **GAA** SAA gln 91 CAA AGA arg/ AAA lys / TTG leu / CAA gln GAT 31 CTA leu 91 GAT asp 151 GCT ala 211 AAG 1ys 271 GAA GAA glu 831 GAT CAA GAA glu CAA gln CTT CAA CAA AGC ( GAA glu AGA arg AAA 1ys TTG CAG gln GAG glu TTA CCT 9 ala AAG lys 3AG glu / 1 GAA CAA C GAT asp arg 81 GAA 41. CAA gln 61 CGT glu 101 CAA AGC ser GAA GAA AGA arg AAA Iys ' SA gln 121 171A 16u 181 181 6AG 6CT 6CT 301 1ys

## FIGURE 9A

### TTA leu SAG glu AAA lys TTA leu CAA gln CAA CAA CGT GAT asp AAA lys CGT CAT his GAA glu GAA glu AGA arg AGC ser ACG thr GGT CCA GAT CAA gln CAA gln TTA ATA ile GAG glu TAT GAT TTA leu CAA rTG Leu CAA GCT ala GAA glu TAT GAA glu GAA glu AAG lys AAG lys AGC ser GAT AAG lys TAT GAA glu CAA gln CAA TTA AGG arg GAG glu GGA gly TCC GAT AAA lys CAA GCA ala TTG leu GAT CAA asp CGT AGA arg GAA glu GAA TTA GAA glu ala AAG Lys AGC ser CAA ATA ile AGT GT arg GAA glu CAA TTA AAT asn ser CAA GAA 4AA Lys TTG Leu GAT asp AAT GAT 366 gly 251 CCAA Bgln CCTT CCAA CCAA Bgln CCAA CCAA CCAA CCAA CCAA 391 3AA 3AA 451 451 4GA 4GA 4AA 1ys 571 TTG 1eu 631 CAG CAG 691 glu 751 CTT leu 811 AAC TTA GAG glu GCT ala AAG lys GAG glu AAG 1ys GAA glu GAC asp CAA GAA glu CAA AAA lys GAT CGT SAG AGA AGC GAA glu AGA arg AAA lys TTG leu ser arg

## FIGURE 9B

AAA 1ys ser CAA GAA glu GAT TTA AAA 1ys AAT GAA glu CAA ATA ile ₩ lys phe CAT his ATA ile asp asp TTC GAA glu AAA lys GAT asp GAT GAT AAT GAT GAA ATA ile AAT asn GAA glu AATasn asp AGG arg GAA glu len GAC AAA 1ys **TTA** AAA 1ys GTT val CGA arg ser GAG glu asp TCA TAT ᄓ CAA GAT ser CAA GAT asb GGA gly GAA 77 ser ATA ile TTA asp TTG leu GAA glu GAA CCA ATT GAC GTG val glu pro ile ATT ile GAT GAA glu AAA lys AATasn tyr TAT GTT val GAA glu Z **GTA** pro AAT asn ATA ile GAA glu CCT val ser glu thr 351 ACA\_ CCT ala lys CTA leu AAA TCA TTT AAG ser thr ser 371 phe 391 glu 411 gly 331 GAG GAA AGT lys asp 991 / ACA TTA thr leu 1051 / GAA ATA glu ile tyr lys 1231 / ATA GAA GAA glu AAA asp { 1171 GAC AT GAA glu AAG 1ys GAT TTA ATT ile GGA CAT his asp GGA gly AGA GAA AAT asn GAG glu GAC GAA glu arg glu lys tyr 8 361 GAT GAA 0 leu glu 321 ATA CAA ile gln 341 AAG TAT AAC ATA asn ile glu AAT TTA GAT asp asn GAA asn i 401 asp 381 841 / GGAA AAA gGu lys 901 / 6GA CAT GGA CAT 6GCT GAC ala asp 11021 / ATA AGT 11081 / 1081 / GGA GAT glu glu 1201 / GAT GAT asp SAA GAA asp glu a 1141

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leu AAA 1ys GAT asp GAA glu ser GTG AGT AAA lys AAG lys ATC ile TAT CAG gln GAT asp GAA glu AATasn AAG lys TTA leu GTT CCA asn pro AAG 1ys AAT GAA glu AAA lys TAA OCH GTT CTA gln phe CAG asn TT AATAAG GAT AAT AAT asn asp lys AAG lys GAC AAA asn asb met GAT GGA gly lys asp a lys asn 471 asb AAA AAT GAC phe TAT tyr lys t 1351 AAA T 1411 l ys AT GAA glu AAA lys phe ATA ile ile 116leu GAT asp TAT tyr glu his . 461 TCA lys TCT GAA AAG AAA GAG CAT ser lys i 441 lys 481 AAA ser tyr asp 1381 / TTC ATA lys gly 1321 / TAT GAT AAA GGA ile TTA leu phe i 1441 GAG 1

### FIGURE 9D

LSN.3'STOP -> 1-phase Translation

CAAGAACAACAA ... ATGAAACTATAA linear 1482 b.p. DNA sequence

GAA GAT asp CAA CGT GAA glu CAA GAA glu AGA arg GAA glu AAA AGC ser lys TTG CTA CAA gln CAA gln GAG glu GCT ala AAG lys CAG gln GAT CAA GAA TTG gln F leu GAG glu GAA glu AAA 1ys AAG 1ys AGC ser AGA arg GAA glu CAA gln CAA GAT TTA GCT ala asp AAA 1ys TTA CAA CAA gln asp GAT CGT arg CGT GCT AAG lys GAA glu GAA glu AGA arg AGC ser GAA glu CAA CAA gln TTA GAG glu GAG AGA AAA lys CAA gln asb arg TTG leu GAT CAA GAA glu mlg GAA glu GCT ala AAG lys AGC ser / 11 GAA CAA ( gln 31 51 GAA gln 91 CAA glu 71 CAA arg AAA lys lys TTG leu CAA gln GAT 31 CTA leu 91 GAT asp 151 GCT 1ys 271 GAA 81u 331 AGC ala 211 AAG ser asp GAA glu CAA gln CAA GAT CTT CAA gln AGC GAA AGA AAA 1ys CAGglu arg TTG gln CAA / GAG glu TTA GCT ala AAG lys 3AG glu ′ 1 GAA CAA asp 41 CAA GAT gln 61 CGT GAA glu 101 CAA arg 81 AGC ser GAA GAA Blu / AGA AAA Ilys / TTA gln 121 TTA TTA 1eu 181 GAG GAG glu 241

## FIGURE 10A

	SA	gln	TTA	len	GAG	glu	ECT.	ala		AAA	7 \		TTA	len		Š	gln	)	ATA	ile
	SA	gln	GAT	asb	SAA	gln	CGT	arg	0	AAA	1 \ S	-	CGT	arg		CAT	his		ATA	ile
	GAA	gln	AGC	ser	GAA	glu	AGA	arg	)	ACG.	thr		<b>GGT</b>	gly		CCA	pro		TCT	ser
	CAA	gln	Š	gln	T	len	GAG	glu	)	GAT	asp	<u>-</u>	TAT	tyr		ATA	ile		ATA	ile
	TTG	len	Y V	gln	GAT	asp	SA V	gln	)	ECT 6CT	ala		TTA	len		TAT	tyr	,	GAA	glu
	AAG	lys	GAA	glu	AGC	ser	GAA	glu	•	AAG	lvs		GAT	asp		TAT	tyr	,	AAG	lys
	GAA	glu	CAA	gln	CAA	gln	TTA	leu		AGG	arg	)	GAG	glu		<b>GGA</b>	gly	,	JCC	ser
	AAA	lys	TTG	len	CAA	gln	GAT	asp	-	CAA	gln	)	GCA	ala		CGT	arg	)	GAT	asp
	_	ala	AAG	lys	GAA	glu	AGC	ser		GAA	-		TTA	len		GAA	glu		AGA	arg
	_	arg	GAA	glu	CAA	gln	_	gln		TTA			-	i le		AAT	asn		AGT	ser
	AGA	arg	AAA	lys	TTG	len	CAA	gln	,	GAT	asp	•	GAT	asb		GAA	glu		AAT	asn
131	GAG	glu 151	GCT	ala 171	AAG	lys 191	GAA	glu	$\bar{2}11$	AGA	arg	231	66A	gly	251	TCA	ser	271	999	gly
\	CAA	gln /	E	len /	GAA	gln/	CAA	gln	_	Š	gln	, ~	CAT	his	\	S	pro	_	AGA	arg
391	GAA	glu 451	AGA	arg 511	AAA	lys 571	TTG	leu	631	CAG	gln	691	GAA	glu	751	E	len	811	AAC	asn
	TTA	len	GAG	glu	GCT	ala										GAA	glu		GAC	asb
	GAT	asb	CAA	gln	CGT	arg	GAA	glu		SA	gln		AAA	lys		ATA	ile		CAG	glu
	AGC	ser	GAA	gln	AGA	arg	AAA	lys		TTG	len		AGA	arg		SCT	ala		$\Box$	pro
121	Š	gln 141	TTA	leu 161	GAG	glu 181	GCT	ala	201	AAG	lys	221	GAA	glu	74 T	SS	pro	261	TTA	len
\	SA	gln /	GAT	asp /	CAA	gln /	ĊĞŢ	arg	_	GAA	gIn	\	T	leu ,	\	ATA	ile	\	TCT	ser
361	GAA	glu 421	AGC	ser 481	GAA	glu 541	AGA	arg	601	AAA	lys	661	AAT	asn	T7/	GAA	gln	781	TCT	ser

# FIGURE 10B

ser CAA GAA glu GAT asp TTA leu AAA lys leu GAA CAA ATAglu asn CAT his AAA 1ys phe AAT ile **GAA** ATA ile GAT GAT asp GAT asp ΔL glu AAA AAA phe lys lys asp ATA AAT GAT GAA glu AAT asn AATasn GAA asp asn glu ile GAT AAA AGG arg AAA 1ys ITA leu GAC asp lys GAA asn GTT val glu AAT CGA CAA asp Ϋ́ GAG glu arg GAT SC ser TAT tyr 7 ser GAT GGA gly GAA asp CAA ATA TTA len TCT ser ile AAA lys GAA GTG GAA GAC <u>1</u>16 CCA ile asp len glu ATT phe asp GAA AAA lys asn GAT glu asn GTT AAT TAT tyr ile ATT AATglu asn GTA GAA GAA ζ AAT ATA ile glu CCT pro ser AAT asn ΑÇ ala AAA TCA GAT AAG lys GAA CTA glu leu ser asp ser glu thr 5 phe 391 lys 431 6AG AGT ser \_\_T GAA leu ile GAA glu lys asp GAA ATA TAT AAA glu thr tyr 1231 asp <sub>1</sub> 1051 lys 991 ACA glu GAC hr GAA glu AAG lys CAT his asp TTA **GGA** GAT leu ATT ile gly **GAA** glu AGA GAA glu AAT asn GAG asp 66Agly GAA arg glu GAC glu TAT CAA gln lys tyr 361 GAT GAA glu asn AAC ATA asb AAG TAT asn ile TTA GAT AAG AAA lys asp 381 len leu 321 ATA ile ile ser 1081 / GAA GAT glu asp 1141 / asp GAA GAA glu asp nis / GAC ATA AGT GAT GAT AAA GGA 1021 1201 GAA glu 901 GGA gly gly 6CT ala

## FIGURE 10C

AAA 1ys GAT GAA glu GTG val AAG lys ATC ile TAT GAA glu CAG gln ATA ile AAG 1ys TTA GTT AAT asn ATT ile AAG 1ys GTT val GAA glu TAA OCH CAG gln AAT CTA leu AAG ( GAC AAA 1ys GAT ATG asb GGA gly asn asb phe GAC AAA AAT phe 491 lys a TAT 1351 / AAA TAT ATA ile / AAA lys t 1411 his 1 1471 YY. AAA 1ys TTT ATA ile GAT TTG leu ATT ile 441 GAG CAT , glu his 461 ser CT GAA er . GAT ATA ile TTA leu asp / tyr a 1381 TTC A phe 1 1441 GAG 1 glu 1

# FIGURE 10D